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AMENDMENTS TO THE SPECIFICATION

Amendment to the title of the invention

Please delete current title of the invention "NOVEL PROTEIN", and replace it with the following:

NOVEL SECRETORY OR MEMBRANE PROTEIN EXPRESSED IN SKELETAL MUSCLES

Amendment to the Abstract

Please delete current Abstract and replace it with the following:

The present invention provides a novel secretory or membrane protein expressed specifically in skeletal muscles, a nucleic acid encoding the same, an antibody against the same, useful as a prophylactic/therapeutic agent or diagnostic agent for a disease associated with an abnormality of differentiation of skeletal muscle cell or metabolism function, or as a tool for screening a drug-candidate compound effective for the prophylaxis/treatment of the disease.

Amendment to the description in the specification

Please delete the paragraph on page 15, line 26 to page 16, line 24, and replace it with the following paragraph:

The protein of the present invention is a secretory or membrane protein, and is translated as a precursor polypeptide having a signal peptide at the N-terminus in vivo, and then undergoes processing by signal peptidase to become a mature protein. The cleavage site of the signal peptide (N-terminus of the mature protein) can be determined by, for example, subjecting the fully or partially purified protein of the resent invention to Edman degradation, and can be estimated from the primary structure of the precursor polypeptide using a known mathematic algorithm. Such algorithms include, for example, but are not

limited to, the algorithm described in Nielsen et al., Int. Neural Syst., 8 (5-6): 581-599 (1997) [the algorithm is incorporated in the Signal P program (~~available on the WWW server: http://www.cbs.dtu.dk/services/SignalP/~~)published in, e.g., *Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites*, Henrik Nielsen, Jacob Engelbrecht, Søren Brunak and Gunnar von Heijne, Protein Engineering, 10:1-6, 1997; *Improved prediction of signal peptides: SignalP 3.0*, Jannick Dyrløv Bendtsen, Henrik Nielsen, Gunnar von Heijne and Søren Brunak, Mol. Biol., 340:783-795, 2004], the algorithm described in Emanuelsson et al., J. Mol. Biol. 300: 1005-1016 (2000) [the algorithm is incorporated in the Target P program (~~available on the WWW server: http://www.cbs.dtu.dk/services/TargetP/~~published in *Predicting subcellular localization of proteins based on their N-terminal amino acid sequence*, Olof Emanuelsson, Henrik Nielsen, Søren Brunak and Gunnar von Heijne, J. Mol. Biol., 300: 1005-1016, 2000)] and the like. For example, when the SOSUI (Signal) program (~~available on the WWW server: http://sosui.proteome.bio.tuat.ac.jp/cgi-bin/sosui.cgi?/sosuisignal/sosuisignal_submit.html/~~published in, e.g., *SOSUIsignal: Software System for Prediction of Signal Peptide and Membrane Protein*, Gomi M., Akazawa F., Mitaku S., Genome Informatics, 11 414-415 (2000); High performance system for signal peptide prediction: SOSUIsignal, Gomi M., Sonoyama M., and Mitaku S., Chem-Bio Info. J., 4 142-147 (2004)) is used, the polypeptide having the amino acid sequence shown by SEQ ID NO:2 or 4 is predicted to be cleaved between Amino Acid No. -1 and Amino Acid No. 1, but this does not always agree with the actual cleavage site, and the signal cleavage position can differ depending on the cell species that expresses the protein of the present invention. Therefore, amino acid sequences having one or two or more amino acids added to, or deleted from, the amino acid sequence starting at Amino Acid No. 1 in the amino acid sequence shown by SEQ ID NO:2 or 4 also include amino acid sequences having one or two or more amino acids added to the N-terminus thereof and amino acid sequences having one or two or more amino acids deleted from the N-terminus thereof.